

YKTLRAEQASQEVKNWMTET

QUERY	YKTLRAEQASQEVKNWMTET	C.BW.96BW1210	F-----T-D-----D-	CRF01-AE.TH.93TH25	--V-----T-----
CONSENSUS_A	F-----t-----g-----	C.BW.96BW15B03	F-----T-D-----D-	CRF01-AE.TH.CM240	-----T-----
A.KE.Q23-CXC-CG	F--F----T-D-----D-	C.BW.96BW1626	F-----T-D-----D-	CRF01-AE.TH.TH022	-----T-----
A.SE.SE6594	F-V----T---G-----	C.BW.96BW17A09	F-----T-D-----D-	CRF01-AE.TH.TH047	-----T-----
A.SE.SE7253	F-----T-D-----D-	C.ET.ETH2220	F-----T-D-----D-	CRF02_AG.FR.DJ263	F-----T----R---
A.SE.SE7535	F-----D-----D-----	C.IN.93IN904	F-----T-D-----D-	CRF02_AG.FR.DJ264	F-----T-----
A.SE.SE8131	F-A----T-G---D-	C.IN.93IN905	F-----T-D-----D-	CRF02_AG.NG.IBNG	F-----T-----
A.SE.SE8538	F-A----T-G---D-	C.IN.93IN999	FR-----T-D-----D-	CRF03_AB.RU.KAL15	F-----T-D-----
A.SE.SE8891	F-----T-G-----D-	C.IN.94IN11246	F-----T-D-----D-	CRF04_cpx.CY.94CY0	F-C-----T-----
A.UG.92UG037	F-----T-G-----D-	C.IN.95IN21068	F-----T-D-----D-	CRF04_cpx.GR.97PVC	F-C-----T-----
A.UG.U455	F-----T-D-----D-----	CONSENSUS_D	-----d-----	CRF04_cpx.GR.97PVW	F-C-----T-D-----
CONSENSUS_B	-----D-----	D.CD.84ZR085	-----	AC.ET.E3099G	F-A-----T-D-----
B.AU.AFL28998	-----D-----	D.CD.ELI	-----D-----	AC.IN.21301	F-----T-D-----D-----
B.--NL43E9	-----	D.CD.NDK	-----D-----	AC.RW.92RW009	F-----D-----D-----
B.AU.MBC18	-----T-----	D.CD.Z2Z6	-----G-----	AC.SE.SE9488	F-----T-D-----D-----
B.AU.MBC200	-----	D.UG.94UG1141	-----D-----	AC.ZM.ZAM174-21	F-----T-----D-----
B.AU.MBC925	-----D-----	CONSENSUS_F	F-----T-G---D-	AC.ZM.ZAM184	F-----T-----D-----
B.AU.MBCC54	-----	F.BR.BZ162	F-----T-G---D-	AC.ZM.ZAM716-17	F-----T-D-----D-----
B.AU.MBCC98	-----	F.CD.VI174	F-----T-G---D-	ACD.SE.SE8603	F-----T-----
B.AU.MBCD36	-----	F.RW.VI69	F-----E-T---G---D-	AD.SE.SE6954	-----RD-----
B.CN.RL42	-----D-----	CONSENSUS_F1	F-----?---g---d-	AD.SE.SE7108	F-----T-G---D-----
B.DE.D31	-----T-----	F1.BE.VI850	F-V-----D-G---D-	ADHU.NO.NOGIL3	F-----T-----D-----
B.DE.HAN	-----T-----	F1.BR.93BR020.1	F-----T-G---D-	ADU.CD.MAL	F-----T-----
B.ES.89SP061	-----	F1.FI.FIN9363	F-A-----T-G---D-	AG.NG.G3	F-----T-----D-----
B.FR.HXB2	-----	F1.FR.MP411	F-----S-----	AG.SE.SE7812	F-----T-D-----
B.GA.OYI	-----D-----	CONSENSUS_F2	F-----T-?------	AGH.U.GA.VI354	F-----T-----
B.GB.CAM1	-----	F2.CM.MP255	F-----T-----	AGJ.AU.BFP90	F-----T-----D-----
B.GB.MANC	-----	F2.CM.MP257	F-----T-G-----	AGJ.ML.95ML8	F-----T-----D-----
B.JP.JH31	-----	CONSENSUS_G	F-----T-G---D-	AGU.CD.Z321	F-----T-G---D-----
B.NL.3202A21	-----	G.BE.DRCBL	F-----T-S---D-	BF.BR.93BR029.4	-----T-D-----
B.TW.LM49	-----T---D-----	G.FI.HH8793	F-----T-G---D-	DF.CD.VI961	-----D-----
B.US.85WCIPR54	-----	G.NG.92NG083	F-----T-G---D-	U.CD.VI1126	F-----T-----D-----
B.US.AD8	-----	G.SE.SE6165	F-C-----D-G---D-	CONSENSUS_CPZ	-----?-----
B.US.BC	-----	CONSENSUS_H	F-----T-D-----D-	CPZ.CD.CPZANT	-----I-----P-A-----
B.US.DH123	-----	H.BE.VI991	FRV-----T-D-----D-	CPZ.GA.CPZGAB	-----D-----
B.US.JRCSF	-----T-----	H.BE.VI997	F-----T-----D-----	CPZ.US.CPZUS	-----P-T-----
B.US.JRFL	-----	H.CF.90CF056	F-----T-D-----		
B.US.MNCG	-----RT--	CONSENSUS_J	F-A-----T-D-----D-		
B.US.NC7	-----	J.SE.SE9173	F-A-----T-D-----D-		
B.US.NY5CG	-----	J.SE.SE9280	F-A-----T-D-----D-		
B.US.P896	-----	CONSENSUS_K	f-----T-----?-		
B.US.RF	-----D-----	K.BE.VI325	F-----T-----D-----		
B.US.SF2	-----D-----	K.CD.EQTB11C	FRV-----T-----		
B.US.WC001	-----	K.CM.MP535	F-----T-----D-----		
B.US.WEAU160	-----T-----	N.CM.YBF30	-----T-----		
B.US.WR27	-----	CONSENSUS_O	-----T-----		
B.US.YU2	-----	O.CM.ANT70C	-----T-----		
CONSENSUS_C	F-----t-d-----d-	O.CM.MVP5180	-----T-----		
C.BR.92BR025	F-----T-D-----D-	CRF01-AE.CF.90CF40	F-----T-----		
C.BW.96BW01B22	F-----T-D-----D-				
C.BW.96BW0402	F-----ST-----D-----				
C.BW.96BW0502	F-----T-D-----D-----				
C.BW.96BW1104	F-----S-----D-----				

Study Subject ID:01RCH85

Study Subject Clone:

Study Subject HLA:A33,A19,B44,B58,Cw7,Cw16

Sequence: Known reactive 20Mer0: YKTLRAEQASQEVKNWMETET p24(169–188)

Possible HLA

A19 A*7403
A33 A*3301,A*3303
B44 B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
B58 B*5801,B*5802
Cw7 Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(8-16) QASQEVKNW B*5801
(9-16) ASQEVKNW B*5801

Anchor Residues Searched

B44 X[E]XXXXXX[Y]
B44 X[E]XXXXX[Y]
B44 X[E]XXXXXXX[Y]
B*4402 X[E]XXXXXX[FY]
B*4402 X[E]XXXXX[FY]
B*4402 X[E]XXXXXXX[FY]
B*4403 X[E]XXXXX[YF]
B*4403 X[E]XXXXX[YF]
B*4403 X[E]XXXXXXX[YF]
B*5801 X[AST]XXXXXX[FW]
B*5801 X[AST]XXXXX[FW]
B*5801 X[AST]XXXXXXX[FW]
Cw*0702 XXXXXXXX[YFL]
Cw*0702 XXXXXX[YFL]
Cw*0702 XXXXXXXXX[YFL]

This table lists epitopes that are experimentally observed to be presented by a HLA type carried by the patient, but the defined epitope has substitutions relative to the peptides from your reference strains and so might be missed by your reagents: in HXB2 for Gag, Pol; MN for Env; BRU for Nef, relative to most B clade Sequences in the database:

Protein	Epitope in Database	Epitope in Ref. strain	Epitope in Consensus B	HLA	Notes
p24(15–23)	LSPRTLNAW	ISPRTLNAW	ISPRTLNAW	B57,B58	
p24(108–117)	TSTLQEIQIGWF	TSTLQEIQIGWM	TSTLQEIQIGWM	B*57,B*5801	
p24(108–117)	TSTVEEQQIW	TSTLQEIQIGW	TSTLQEIQIGW	B*5801	
p24(108–117)	TSTVEEQQIW	TSTLQEIQIGW	TSTLQEIQIGW	B58	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402,B44	
Protease(3–11)	ITLWQRPLV	VTLWQRPLV	ITLWQRPLV	A*6802,A*7401,A19	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B*4402	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B44	

Table 1: **p24**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(15–23)	p24()	LSPRTLNAW	HIV-1 exposed seronegative	human(B57,B58)	[Kaul (2000)]
			<ul style="list-style-type: none"> • 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-specific CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women 		
p24(108–117)	p24(240–249 LAI)	TSTLQEIQIGWF	HIV-1 infection	human(B*57,B*5801)	[Goulder (1996)]
			<ul style="list-style-type: none"> • Response to this epitope was found in 4 slow progressing HLA-B*57 individuals, in 2 it was dominant or very strong • For one donor (from Zimbabwe) this was defined as the optimal peptide • This epitope can be presented in the context of the closely related HLA molecules B*5801 and B*57 		
p24(108–117)	p24(241–250 LAI)	TSTVEEQQIW	HIV-2 infection	human(B*5801)	[Brander & Goulder(2001)]
		<ul style="list-style-type: none"> • C. Brander notes this is a B*5801 epitope 			
p24(108–117)	p24(241–250)	TSTVEEQQIW	HIV-2 infection	human(B58)	[Bertoletti(1998)]
		<ul style="list-style-type: none"> • HIV-2 epitope defined from an infection in Gambia, Bertoletti, Pers. Comm. • All HIV-2 sequences from the database are TSTVEEQIQIW in this region, not TSTVEEQQW as in the paper 			
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402)	[Brander & Goulder(2001)]
		<ul style="list-style-type: none"> • C. Brander notes this is a B*4402 epitope 			
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402,B44)	[Brander & Walker(1997)]
		<ul style="list-style-type: none"> • Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker, C Brander <i>et al.</i>, this database, 1999 			

Table 2: **Protease**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Protease(3–11)	Protease(71–79 LAI)	ITLWQRPLV		human(A*6802,A*7401, ^A Dong (1998)]	
		<ul style="list-style-type: none"> • Predicted on binding motif, no truncations analyzed • Clade A/B/D consensus, S. Rowland-Jones, pers. comm. 			

Table 3: **gp160**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
gp160(31–40)	gp160(30–39 WEAU)	AENLWVTVYY • C. Brander notes this is a B*4402 epitope	HIV-1 infection	human(B*4402)	[Brander & Goulder(2001)]
gp160(31–40)	gp160(30–39 WEAU)	AENLWVTVYY	HIV-1 infection	human(B44)	[Borrow (1997), Goulder (1997), Borrow & Shaw(1998)] <ul style="list-style-type: none"> • Two CTL lines from the patient WEAU were studied – one had an optimal peptide of (A)AENLWVTVYY, and the other (A)AENLWVTVY, and both responded equally well with one or two N-term Alanines • Rapidly post-infection, a strong immunodominant response was observed against this epitope • The naturally occurring forms of the peptide found in WEAU were tested as targets for early WEAU CTLs – the form TENLWVTVY was as reactive as the wild type AENLWVTVY – but the forms AKNLWVTVY, AGNLWVTVY, AANLWVTVY did not serve as targets • The glutamic acid in the second position is a B44 anchor residue • [Goulder (1997)] and [Borrow & Shaw(1998)] are reviews of immune escape that summarizes this study in the context of CTL escape to fixation

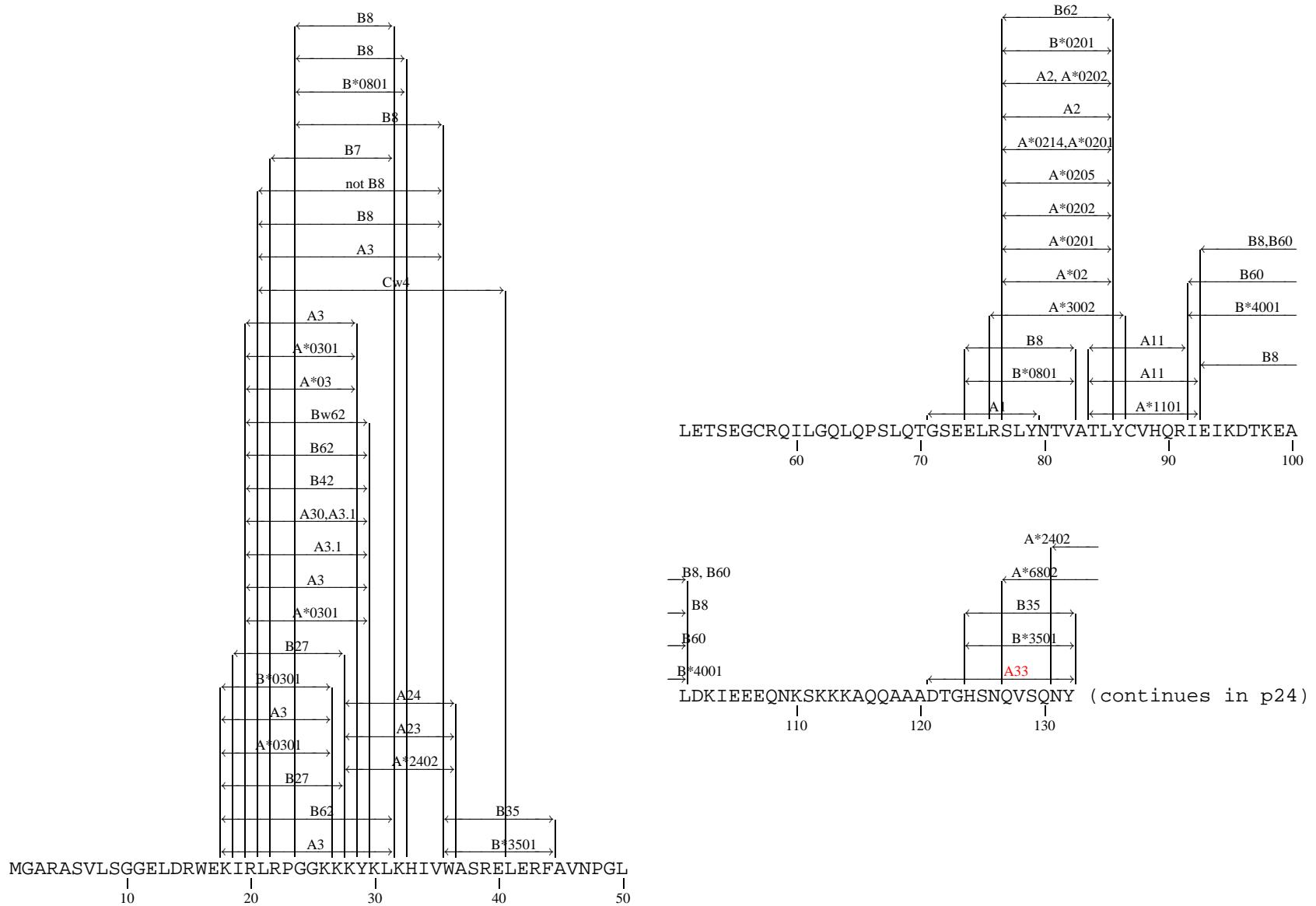
Table 4: All Defined Epitopes within the 20mer, regardless of HLA type

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(173–181)	p24(305–313)	RAEQASQEV	HIV-1 infection	human()	[Lubaki (1997)]
		<ul style="list-style-type: none"> • Eighty two HIV-1-specific CTL clones from 5 long-term non-progressors were isolated and analyzed for breadth of response • A sustained Gag, Env and Nef response was observed, and clones were restricted by multiple HLA epitopes, indicating a polyclonal response • Despite this being a well defined conserved epitope, and thought to be presented by B14, none of the 11 gag-specific clones from a B-14 positive subject could recognize either it or p24 PQDLNTMLN • Thought to be HLA-Cw8 restricted, not B14 as originally reported (C. Brander, B. Walker, and S. Rowland-Jones, personal communication) 			
p24(173–181)	p24(305–313)	RAEQASQEV	HIV-1 infection	human(B14?)	[Price (1995)]
		<ul style="list-style-type: none"> • Study of cytokines released by HIV-1 specific activated CTL • Thought to be HLA-Cw8 restricted, not B14 as originally reported (C. Brander, B. Walker, and S. Rowland-Jones, personal communication) 			
p24(173–181)	p24(305–313)	RAEQASQEV	HIV-1 infection	human(Cw8)	[Johnson (1991)]
		<ul style="list-style-type: none"> • Originally reported as HLA-B14 restricted, but subsequently found not to be presented by cells transfected with B14 • Thought to be HLA-Cw8 restricted (C. Brander and B. Walker) 			
p24(173–181)	p24()	RAEQASQEV	HIV-1 exposure	human(Cw8)	[Rowland-Jones (1998)]
		<ul style="list-style-type: none"> • A CTL response was found in exposed but uninfected prostitutes from Nairobi using previously-defined B clade epitopes that tended to be conserved in A and D clades – such cross-reactivity could protect against both A and D and confer protection in Nairobi where both subtypes are circulating • The A subtype consensus is RAeQAtQEV • The D subtype consensus is RAEQsQdV • Thought to be HLA-Cw8 restricted, not B14 as originally reported (C. Brander, B. Walker, and S. Rowland-Jones, personal communication) 			
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402)	[Brander & Goulder(2001)]
		<ul style="list-style-type: none"> • C. Brander notes this is a B*4402 epitope 			
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402,B44)	[Brander & Walker(1997)]
		<ul style="list-style-type: none"> • Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker, C Brander <i>et al.</i>, this database, 1999 			

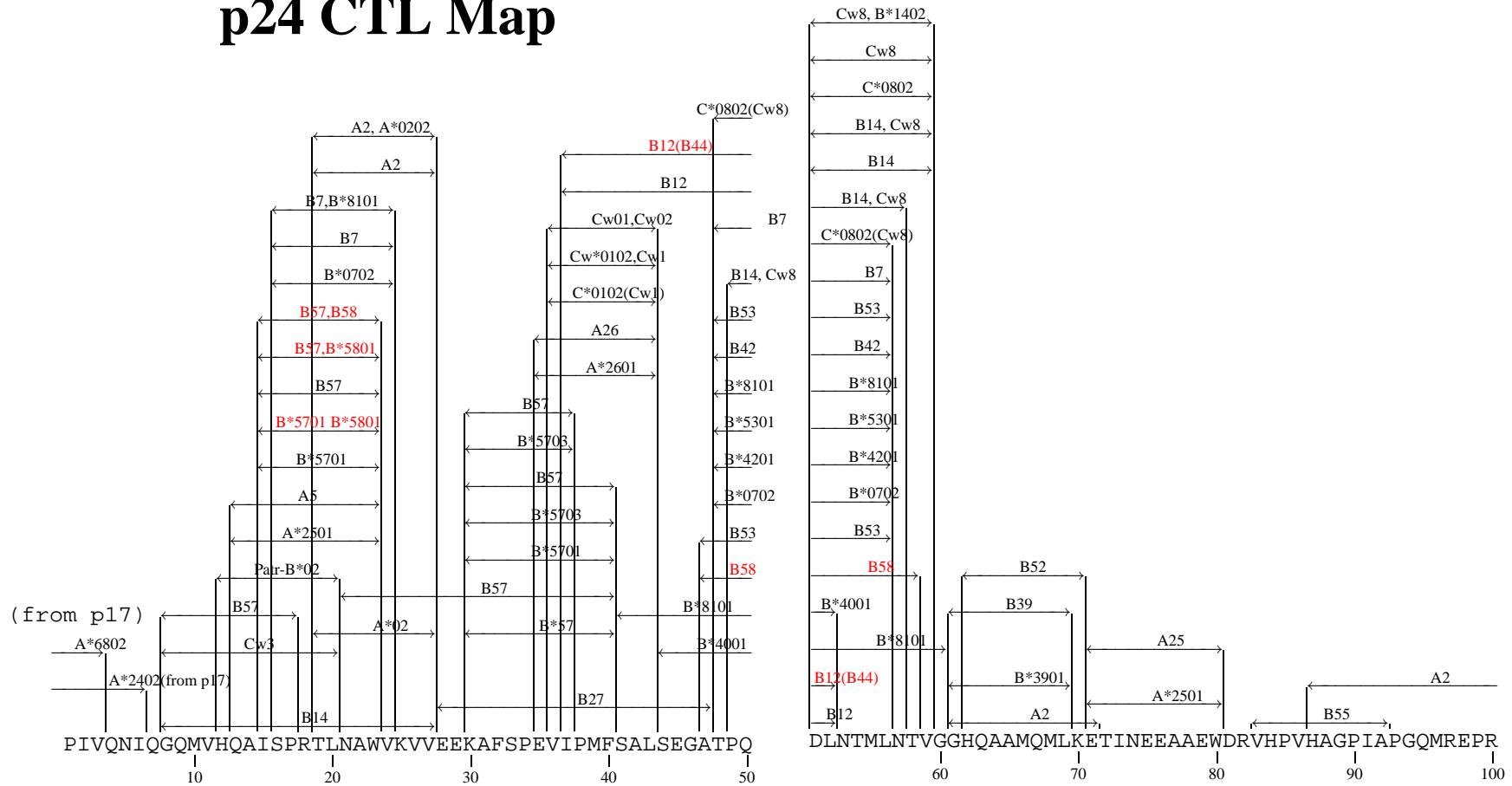
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(174–184)	Gag(306–316)	AEQASQEVKNW	HIV-1 infection	human(B44)	[Brodie (1999)]
		<ul style="list-style-type: none"> • The ability of CTL effector cells was studied by expanding autologous HIV-1 Gag-specific CTL <i>in vitro</i>, and adoptively transferring them • The transferred CTLs migrated to the lymph nodes and transiently reduced circulating productively infected CD4+ T cells, showing that CTL move to appropriate target sites and mediate anti-viral effects 			
p24(174–184)	p24(306–316)	AEQASQEVKNW	HIV infection	human(B44)	[Brodie (2000)]
		<ul style="list-style-type: none"> • Study tracks and quantifies <i>in vivo</i> migration of neo-marked CD8 HIV-specific CTL • Adoptively transferred gene-marked HIV-specific CTL homed to specific lymph node sites, colocalizing within the parafollicular regions of the lymph node adjacent to cells expressing HIV tat-fusion transcripts, indicative of viral replication • The CTL clones expressed CCR5 and localized among HIV-1 infected cells expressing MIP-1alpha and MIP-1beta, CC-chemokines produced at sites of viral replication, suggesting a possible homing mechanism • This study provides a methodology for tracking and studying antigen specific CTL <i>in vivo</i> 			
p24(175–186)	p24(307–318)	EQASQEVKNWMT	HIV-1 infection	human(B44)	[Quayle (1998)]
		<ul style="list-style-type: none"> • HIV is found in semen both as cell-associated and cell-free forms, and HIV-specific CTL could be found in the semen of 5/5 men with CD4 greater than 500 – 3 of the men were analyzed in detail and had broad CTL to gag, env and pol • Two CTL lines from one donor recognized this epitope • Isolation of CTLs specific to HIV in both male and female urinal tracts provide evidence that virus-specific lymphocytes come from the urogenital mucosa, and the authors speculate that CTL in mucosal tissues may be correlated with lower viral load in semen and reduced transmission 			
p24(176–184)	p24(308–316 LAI)	QASQEVKNW	HIV-1 infection	human(B*5301)	[Brander & Goulder(2001)]
		<ul style="list-style-type: none"> • C. Brander notes this is a B*5301 epitope 			
p24(176–184)	p24(309–317 LAI)	QASQEVKNW	HIV-1 infection	human(B*5701)	[Goulder (1996)]
		<ul style="list-style-type: none"> • Recognition of this peptide by two long-term non-progressors • Peptide defined on the basis of B*5801 binding motif, yet not cross-restricted except at high concentrations • Described as B*5701 in C. Brander <i>et al.</i>, this database, 1999 			
p24(176–184)	p24(311–319 LAI)	QASQEVKNW	HIV-1 infection	human(B*5701)	[Brander & Goulder(2001)]
		<ul style="list-style-type: none"> • C. Brander notes this is a B*5701 epitope 			

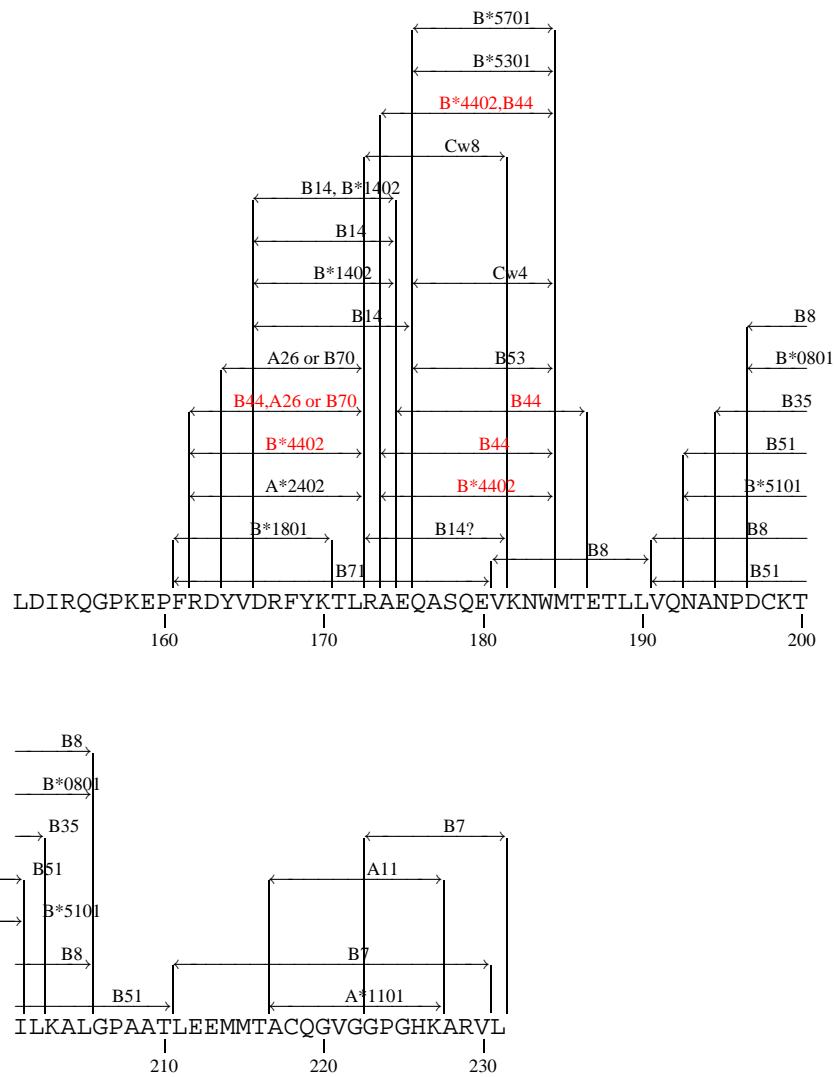
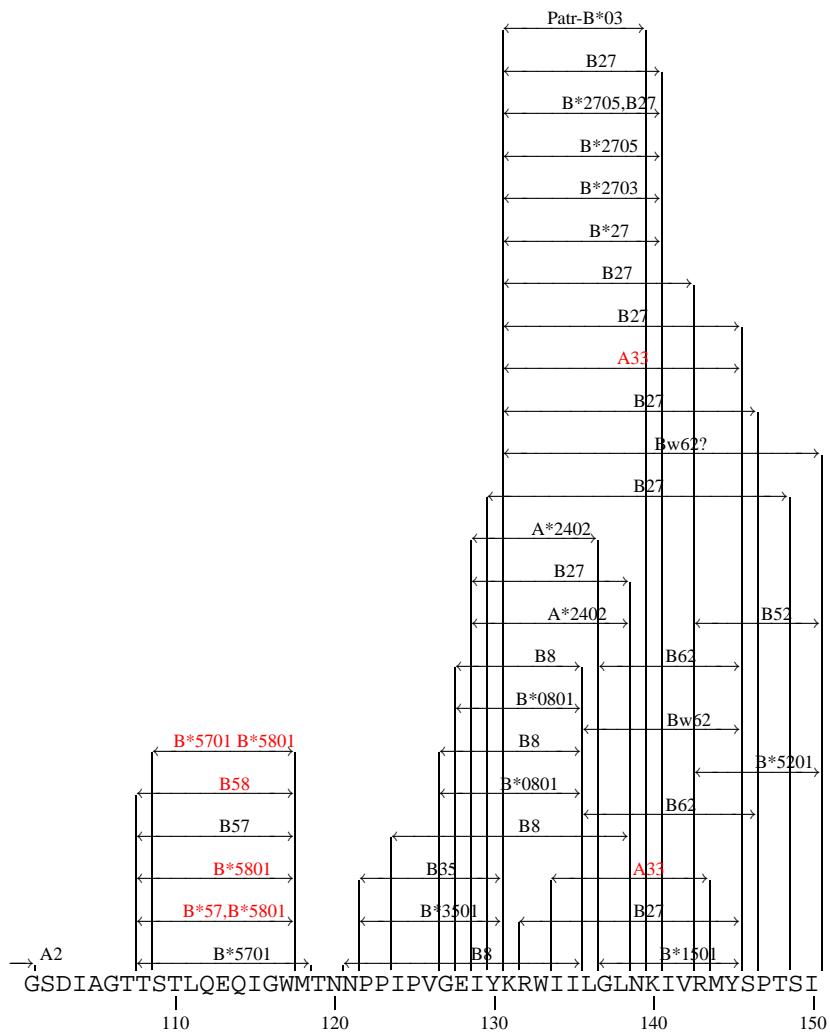
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(176–184)	p24(308–316 LAI)	QASQEVKNW	HIV-1 infection	human(B53)	[Buseyne (1997)]
		<ul style="list-style-type: none"> • Minimal sequence determined through epitope mapping • This is a relatively conserved epitope • HLA-Cw*0401 was defined as the restricting element, but cells that carry Cw*0401 varied in their ability to present this epitope – this could be the result of diminished cell-surface expression of Cw*0401 in some cells • The HLA presenting molecule for this epitope was originally described as Cw*0401, but subsequent experiments with an HLA B53+ C4- cell line and with C1R cells transfected with HLA-B53 have shown that the HLA restricting element is HLA-B53 (Pers. Comm., Dr. Florence Buseyne, 2000) 			
p24(176–184)	()	QASQEVKNW		(B53)	[Brander & Goulder(2001), Buseyne (1996), Buseyne (1997), Buseyne(1999)]
p24(176–184)	()	QASQEVKNW		(Cw4)	[Brander & Goulder(2001), Buseyne (1997), Buseyne(1999)]

p17 CTL Map



p24 CTL Map





p2p7p1p6 CTL Map

AEAMSQVTNSATIMMQRGNFRNQRKIVKCFNCGKEGHTARNCRAPRKKG
 10 20 30 40 50

p2 <- start p2 end <> p7 start

WKCGKEGHQM**A2**KDCTERQANFLGKIWPSYKGRPGNFLQSRPEPTAPPEESF
 60 70 80 90 100

<> p7 end p1 start p1 <> p6 start
 end

RSGVETTTPPKQEPIDKELYPLTSRLSLFGNDPSSQ
 110 120 130

p6 end ->

Protease CTL Map

A*7401
 A*6802,A*7401,A19
 A*6802

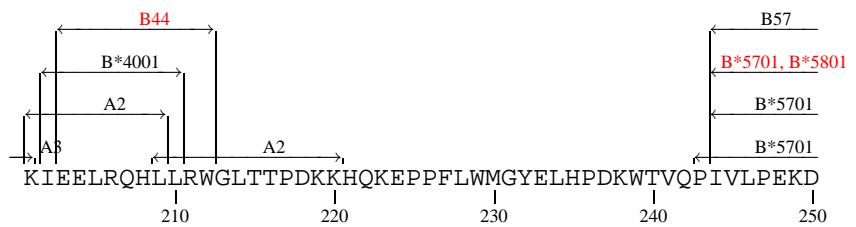
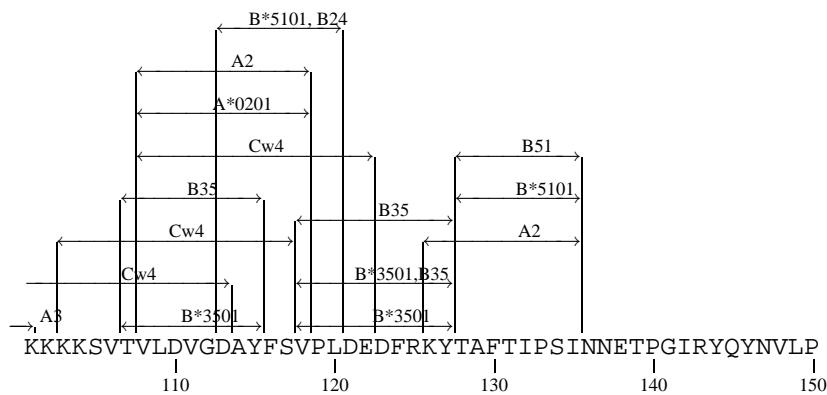
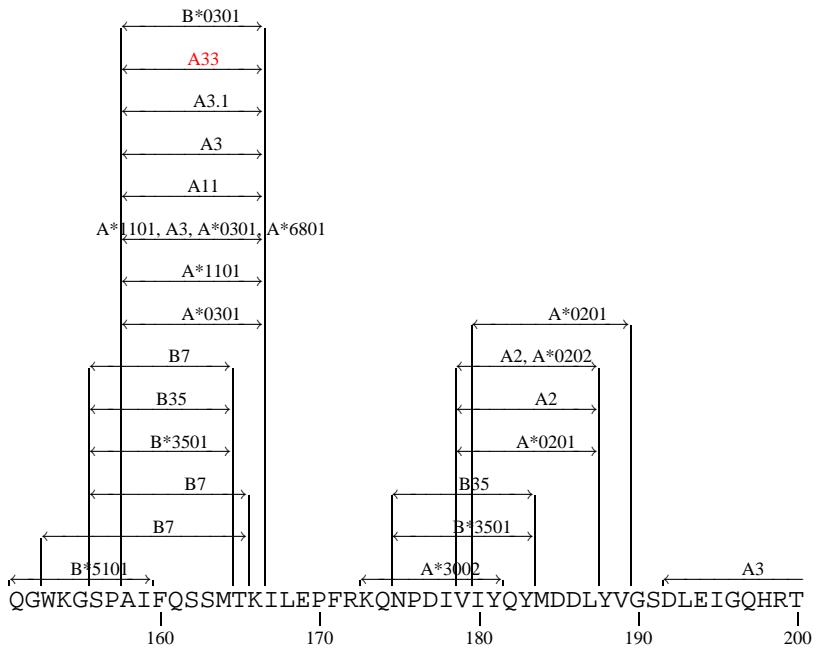
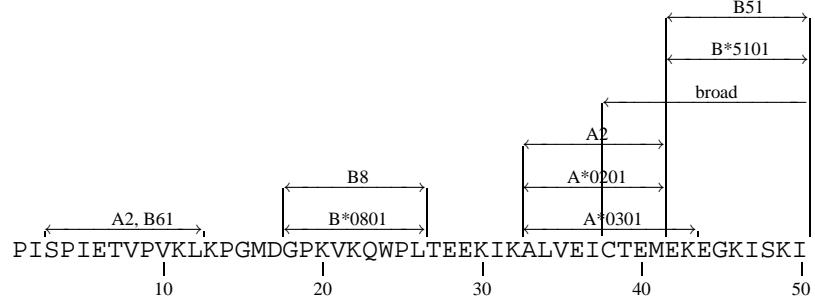
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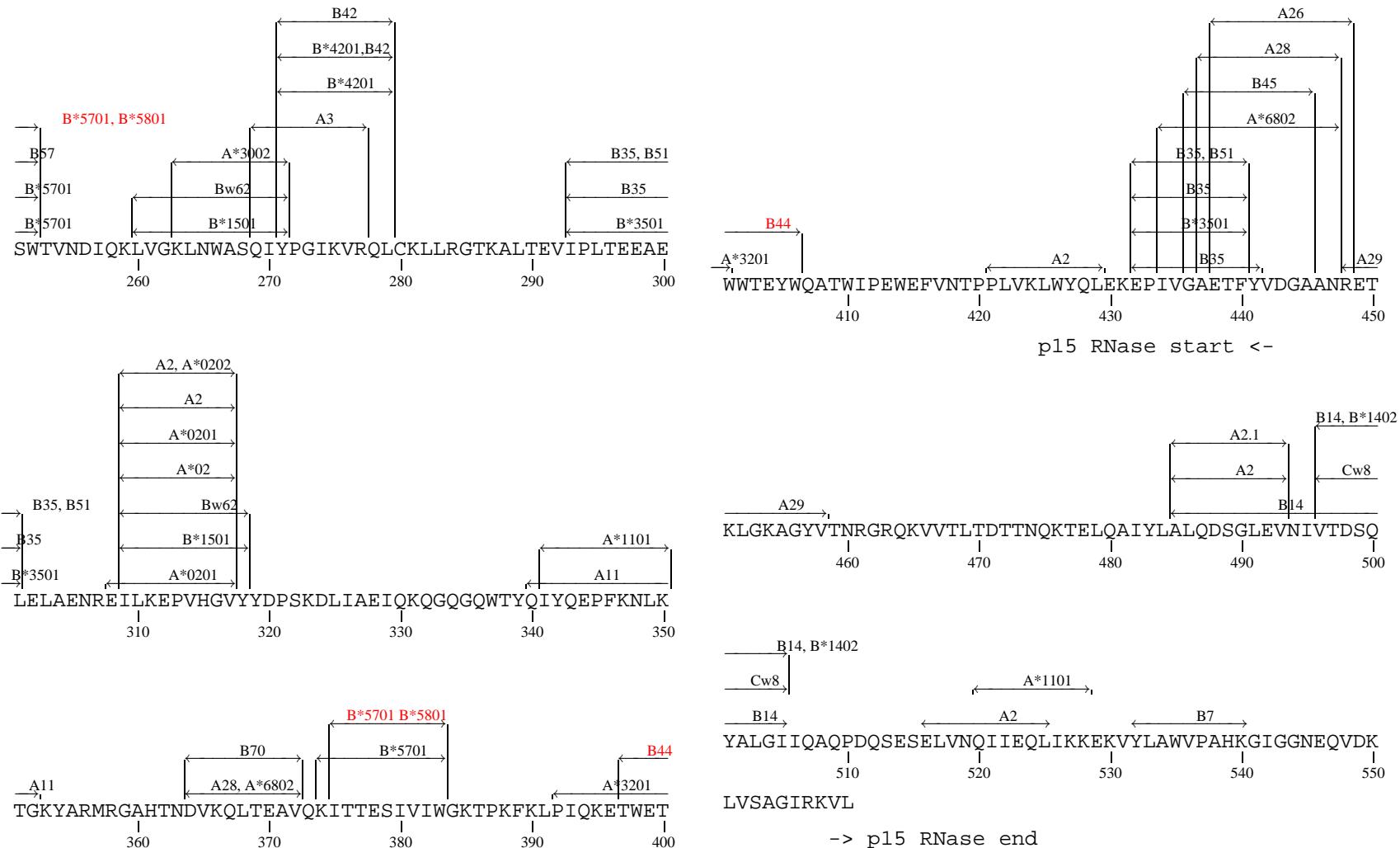
A*6802

GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
 60 70 80 90

A*0201

RT CTL Map





Integrase CTL Map

FLDGIDKAQDEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAM
 10 20 30 40 50

HGVDCSPGIWOLDCTHLEGKVILVAVHVASYIEAEVIPAETGQETAYF
 60 70 80 90 100

^{A*6802}
 LLKLAGRWPVKTIHTDNGSNFTGATVRAACWWAGIKQEFGIPYNPQSQGV
 110 120 130 140 150

VESMNKEKKIIGQVRDQAELKTAQMAVFIHNFKRKGIGGYSAGERI
 160 170 180 190 200

VDIIATDIQTKELEKQKITKIQNFRVYYRDSRNPLWKGP
 A2
 A*0201
 210 220 230 240 250

IQDNSDIKVVPRRKAKIIRDYKGKQMAGDDCVASRQDED
 260 270 280

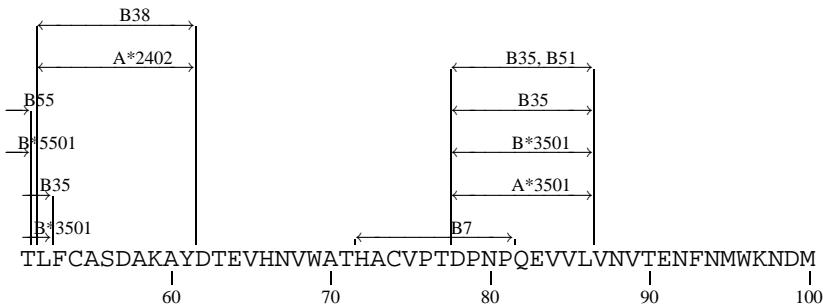
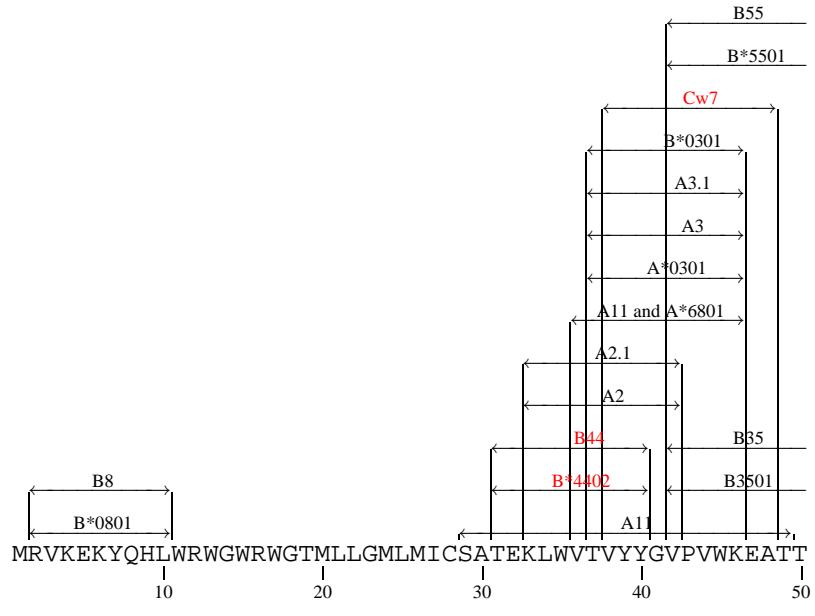
Rev CTL Map

MAGRSGDSDEELIRTVRLIKLLYQSNNPPNPEGTRQARRNRRRWERQR
 10 20 30 40 50

^{B*5801}
 Cw5
 B14, Cw8
 B14
 A1
 QIHSISERILGTYLGRSAEPVPLQLPPLERLTLD
 CNEDCGTSGTQGVGSP
 60 70 80 90 100

QILVESPTVLESgtKE
 110

gp160 CTL Map

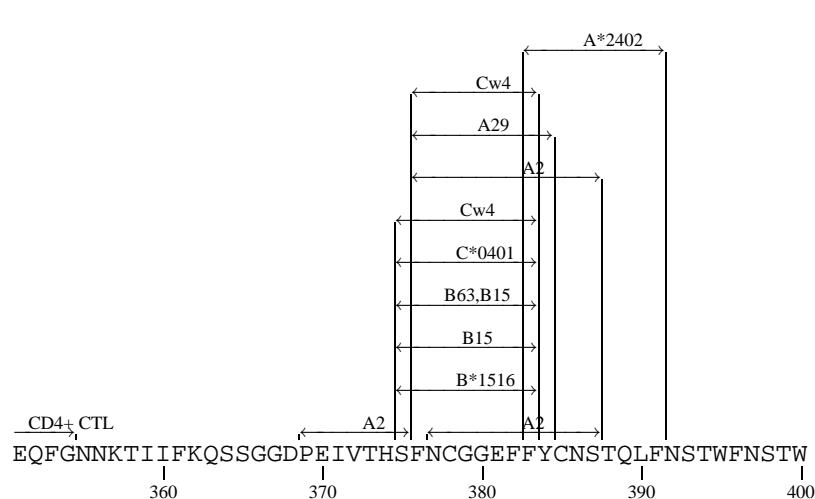
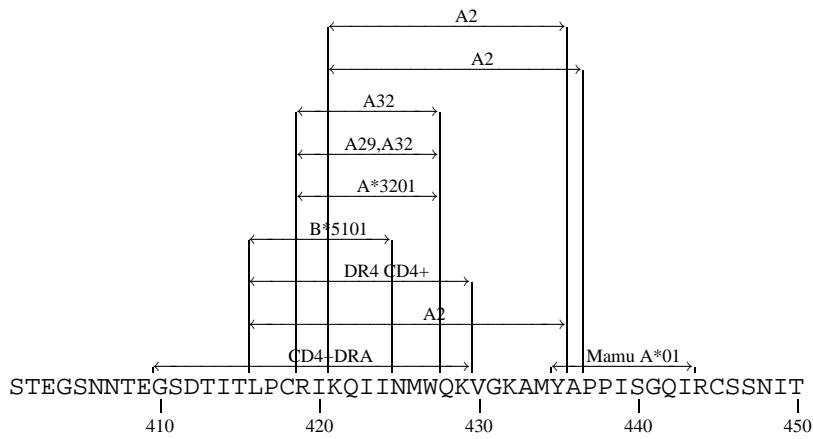
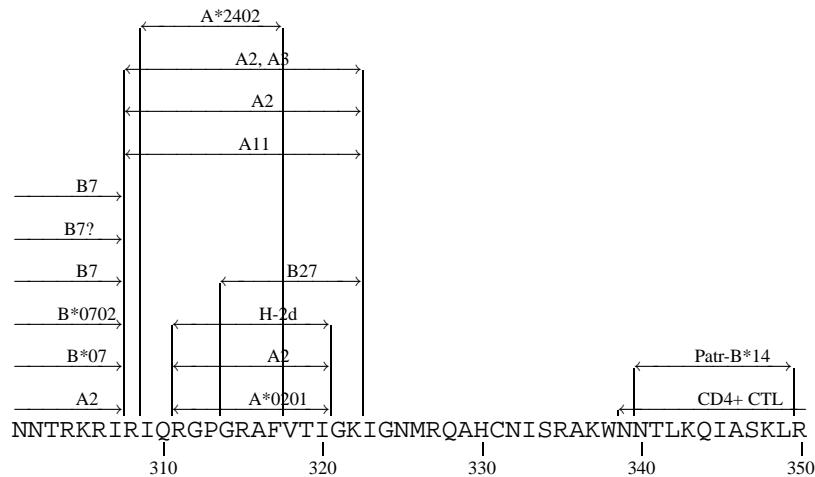


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110 120 130 140 150

A2.1
A2
Cw8
Cw*08
KGEIKNCSFNISTSIRGVQKEYAFFYKLDIIPIDNDTTSYKLTSCNTSV
160 170 180 190 200

A2
A2.1
A2
A2.1
ITQACPKVSFEPPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHG
210 220 230 240 250

B7
B7?
B7
B*0702
B*07
A2
B35
B*3501
B7
IRPVVSTQLLNGLSAAEEEVIRSVNFTDNAKTIIVQLNTSVEINCTRPN
260 270 280 290 300



Peptides from position 460 to 500:

- A2 (460-500)

Sequence: GLLLTRDGGNSNNESEIFRPGGDMRDNRSELYYKYKVVKIEPLGVAPTK

Positions: 460, 470, 480, 490, 500

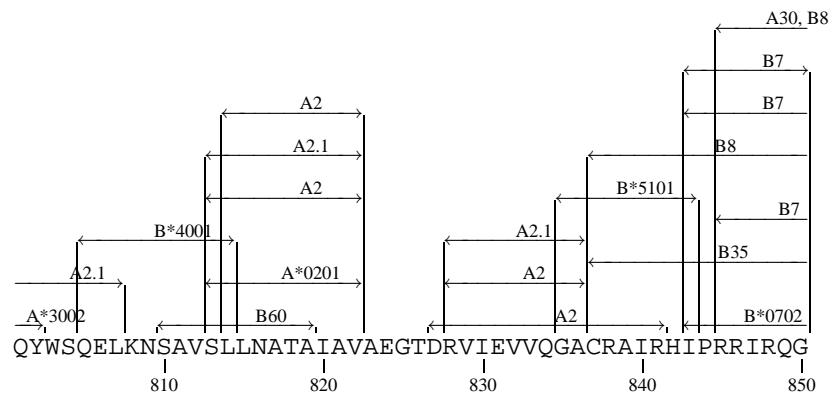
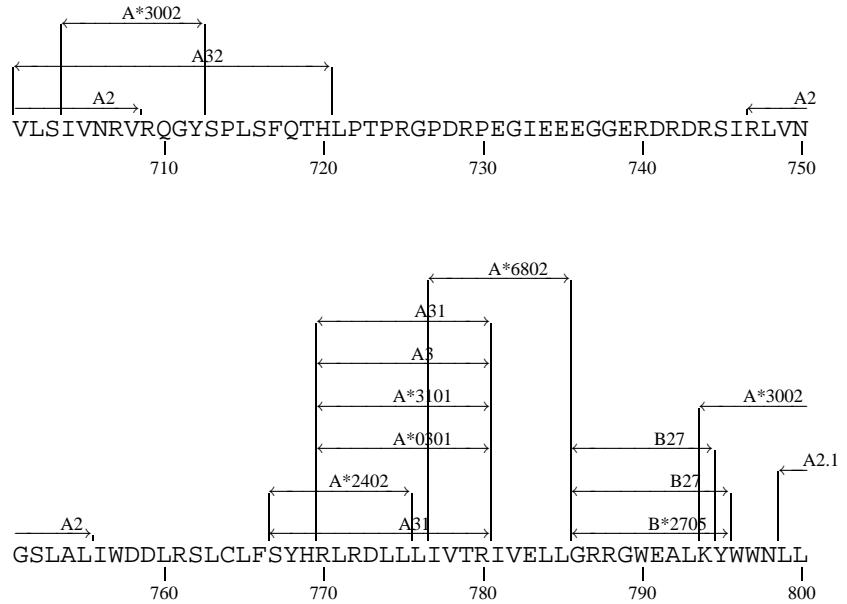
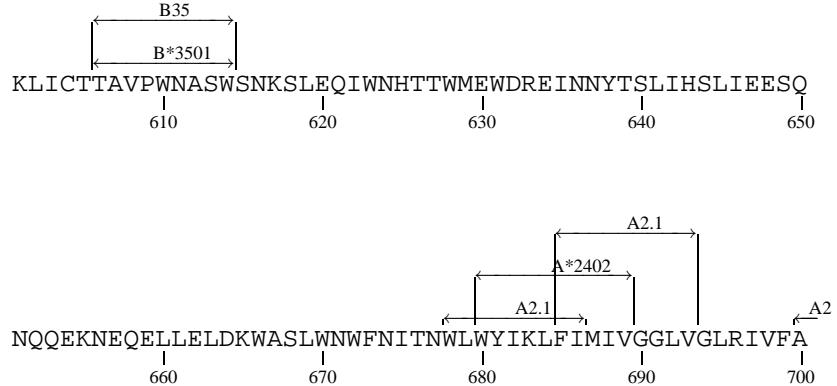
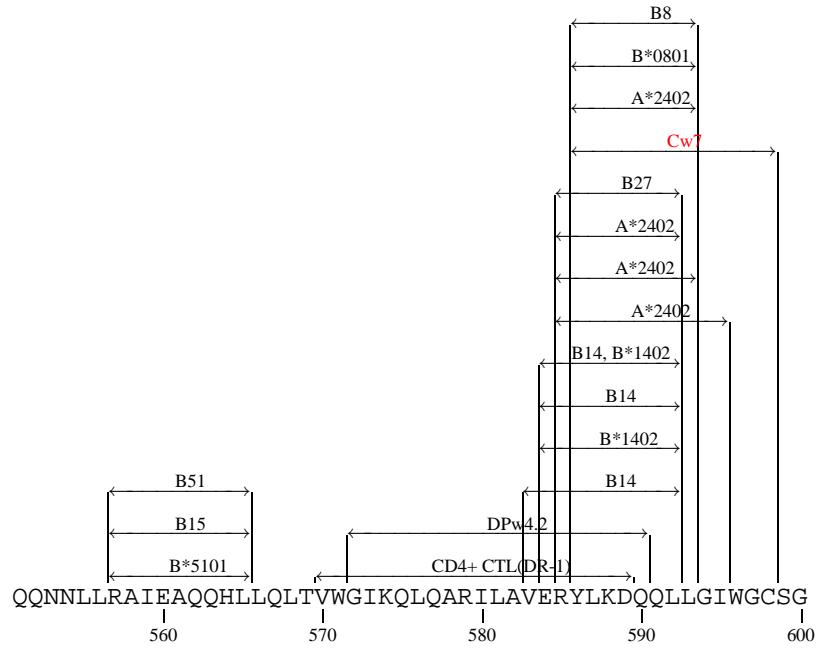
Peptides from position 510 to 550:

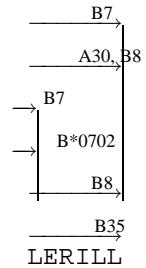
- A2 (510-550)

Sequence: AKRRVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQLLSGIVO

Positions: 510, 520, 530, 540, 550

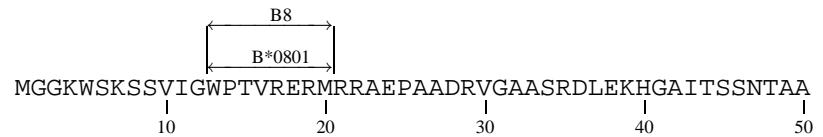
gp120 end <> gp41 start

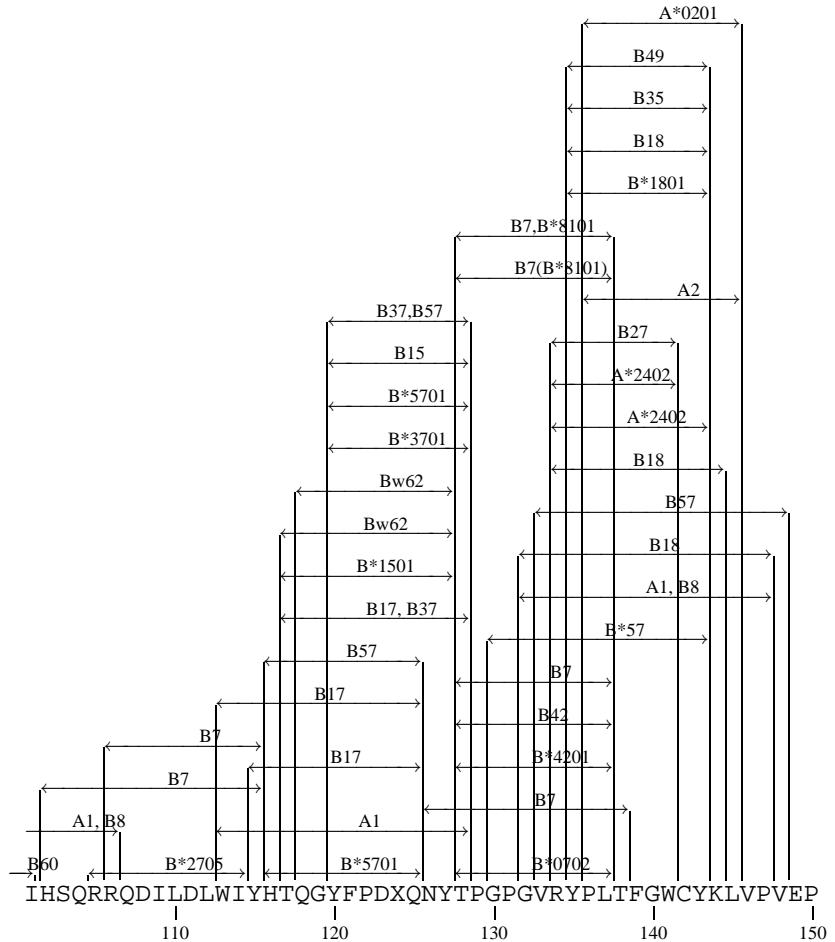
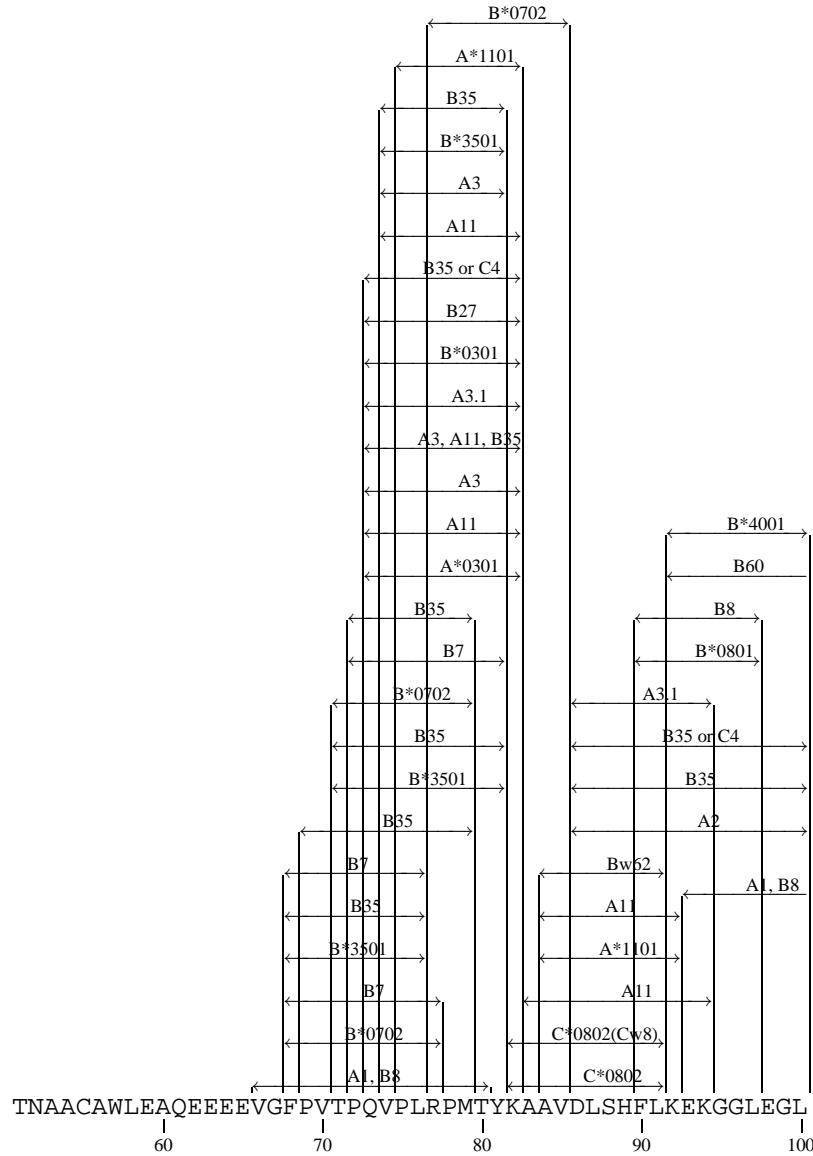


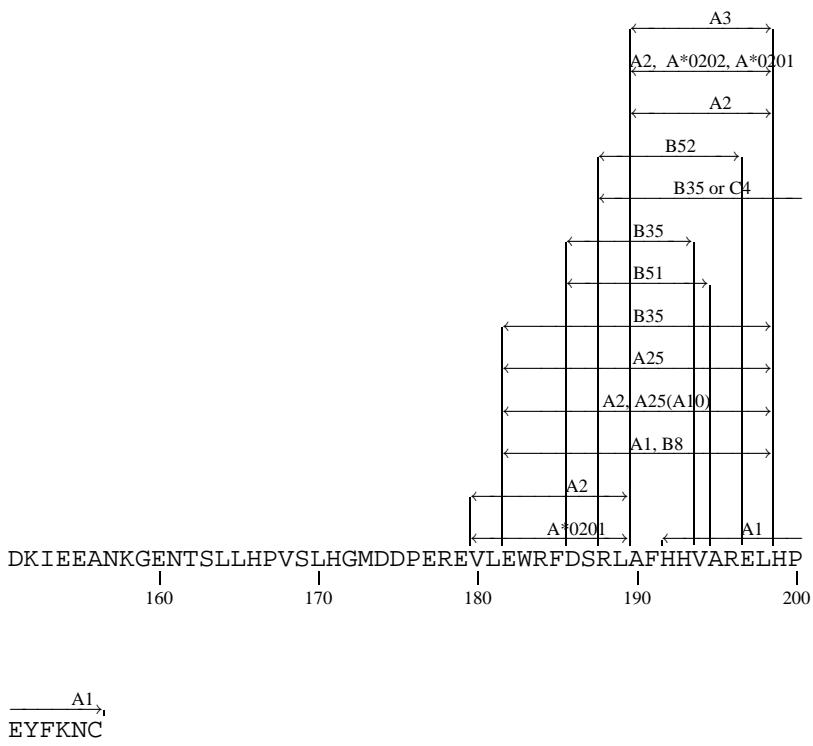


-> gp41 end

Nef CTL Map







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